



20093A-21US-Substitute Sequence Listing.txt
SEQUENCE LISTING

<110> Murphy, Gerald P.
Boynton, Alton L.
Sehgal, Anil

<120> Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS
FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS

<130> 20093A-002100US

<140> 09/301,380

<141> 1999-04-27

<150> 60/112,098

<151> 1998-12-14

<150> 60/083,152

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<170> PatentIn Ver. 2.0

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<212> DNA

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1 5 10

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Ile Leu Phe Leu Cys Gln Met Ile Ser Ala Leu Glu Val Pro Leu Asp
15 20 25 30

cca aaa ctt ctt gaa gac ttg gta cag cct cca acc atc acc caa cag 267
Pro Lys Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile Thr Gln Gln
35 40 45

tct cca aaa gat tac att att gac cct cgg gag aat att gta atc cag 315
Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln
50 55 60

tgt gaa gcc aaa ggg aaa ccg ccc cca agc ttt tcc tgg acc cgt aat 363
Cys Glu Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp Thr Arg Asn
65 70 75

ggg act cat ttt gac atc gat aaa gac cct ctg gtc acc atg aag cct 411
Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro
80 85 90

ggc aca gga acg ctc ata att aac atc atg agc gaa ggg aaa gct gag 459
Gly Thr Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly Lys Ala Glu
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			130					135					140			
acc	aaa	gaa	aaa	ctt	gaa	cca	atc	aca	ctt	caa	agt	ggt	cag	tct	tta	603
Thr	Lys	Glu	Lys	Leu	Glu	Pro	Ile	Thr	Leu	Gln	Ser	Gly	Gln	Ser	Leu	
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Val	Leu	Pro	Cys	Arg	Pro	Pro	Ile	Gly	Leu	Pro	Pro	Pro	Ile	Ile	Phe	
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Trp	Met	Asp	Asn	Ser	Phe	Gln	Arg	Leu	Pro	Gln	Ser	Glu	Arg	Val	Ser	
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caa	ggt	ttg	aat	ggg	gac	ctt	tat	ttt	tcc	aat	gtc	ctc	cca	gag	gac	747
Gln	Gly	Leu	Asn	Gly	Asp	Leu	Tyr	Phe	Ser	Asn	Val	Leu	Pro	Glu	Asp	
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acc	cgc	gaa	gac	tat	atc	tgt	tat	gct	aga	ttt	aat	cat	act	caa	acc	795
Thr	Arg	Glu	Asp	Tyr	Ile	Cys	Tyr	Ala	Arg	Phe	Asn	His	Thr	Gln	Thr	
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ata	cag	cag	aag	caa	cct	att	tct	gtg	aag	gtg	att	tca	gtg	gat	gaa	843
Ile	Gln	Gln	Lys	Gln	Pro	Ile	Ser	Val	Lys	Val	Ile	Ser	Val	Asp	Glu	
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Leu	Asn	Asp	Thr	Ile	Ala	Ala	Asn	Leu	Ser	Asp	Thr	Glu	Phe	Tyr	Gly	
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Ala	Lys	Ser	Ser	Arg	Glu	Arg	Pro	Pro	Thr	Phe	Leu	Thr	Pro	Glu	Gly	
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aat	gca	agt	aac	aaa	gag	gaa	tta	aga	gga	aat	gtg	ctt	tca	ctg	gag	987
Asn	Ala	Ser	Asn	Lys	Glu	Glu	Leu	Arg	Gly	Asn	Val	Leu	Ser	Leu	Glu	
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Cys	Ile	Ala	Glu	Gly	Leu	Pro	Thr	Pro	Ile	Ile	Tyr	Trp	Ala	Lys	Glu	
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Asp	Gly	Met	Leu	Pro	Lys	Asn	Arg	Thr	Val	Tyr	Lys	Asn	Phe	Glu	Lys	
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Cys	Ile	Ala	Lys	Asn	Ala	Leu	Gly	Ala	Ile	His	His	Thr	Ile	Ser	Val	
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Arg	Val	Lys	Ala	Ala	Pro	Tyr	Trp	Ile	Thr	Ala	Pro	Gln	Asn	Leu	Val	
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gcc Ala	cct Pro 400	gat Asp	gac Asp	ccc Pro	agc Ser	aga Arg 405	aaa Lys	ata Ile	gat Asp	ggc Gly	gat Asp 410	acc Thr	att Ile	att Ile	ttt Phe	1371
tca Ser 415	aat Asn	gtt Val	caa Gln	gaa Glu	aga Arg 420	tca Ser	agt Ser	gca Ala	gta Val	tat Tyr 425	cag Gln	tgc Cys	aat Asn	gcc Ala	tct Ser 430	1419
aat Asn	gaa Glu	tat Tyr	gga Gly	tat Tyr 435	tta Leu	ctg Leu	gca Ala	aac Asn	gca Ala 440	ttt Phe	gta Val	aat Asn	gtg Val	ctg Leu 445	gct Ala	1467
gag Glu	cca Pro	cca Pro	cga Arg 450	atc Ile	ctc Leu	aca Thr	cct Pro	gca Ala 455	aac Asn	aca Thr	ctc Leu	tac Tyr	cag Gln 460	gtc Val	att Ile	1515
gca Ala	aac Asn	agg Arg 465	cct Pro	gct Ala	tta Leu	cta Leu	gac Asp 470	tgt Cys	gcc Ala	ttc Phe	ttt Phe	ggg Gly 475	tct Ser	cct Pro	ctc Leu	1563
cca Pro	acc Thr 480	atc Ile	gag Glu	tgg Trp	ttt Phe	aaa Lys 485	gga Gly	gct Ala	aaa Lys	gga Gly	agt Ser 490	gct Ala	ctt Leu	cat His	gaa Glu	1611
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gtt Val	gac Asp	aag Lys	gat Asp	cat His 595	cta Leu	gtg Val	gta Val	gct Ala	gat Asp 600	gtc Val	agt Ser	gac Asp	gat Asp	gac Asp 605	agc Ser	1947
ggg Gly	acc Thr	tac Tyr	acg Thr 610	tgt Cys	gtg Val	gcc Ala	aac Asn	acc Thr 615	act Thr	ctg Leu	gac Asp	agc Ser	gtc Val 620	tcc Ser	gcc Ala	1995
agc Ser	gct Ala	gtg Val 625	ctt Leu	agc Ser	gtt Val	gtt Val	gct Ala 630	cct Pro	act Thr	cca Pro	act Thr	cca Pro 635	gct Ala	ccc Pro	gtt Val	2043
tac Tyr	gat Asp 640	gtc Val	cca Pro	aat Asn	cct Pro	ccc Pro 645	ttt Phe	gac Asp	tta Leu	gaa Glu	ctg Leu 650	aca Thr	gat Asp	caa Gln	ctt Leu	2091

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cag Gln	ctg Leu	aag Lys 705	ctg Leu	tct Ser	cct Pro	tac Tyr	gtg Val 710	aac Asn	tac Tyr	tcc Ser	ttc Phe	cgc Arg 715	gtg Val	atg Met	gca Ala	2283
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tac Tyr 880	tat Tyr	tgg Trp	aag Lys	acc Thr	cag Gln	agt Ser 885	tca Ser	tct Ser	aaa Lys	aga Arg	aac Asn 890	aga Arg	cgt Arg	cac His	att Ile	2811
gag Glu 895	aaa Lys	aag Lys	atc Ile	ctc Leu	acc Thr 900	ttc Phe	caa Gln	ggc Gly	agc Ser	aag Lys 905	act Thr	cat His	ggc Gly	atg Met	ttg Leu 910	2859
ccg Pro	ggg Gly	cta Leu	gag Glu	ccc Pro	ttt Phe	agc Ser	cac His	tac Tyr	aca Thr	ctg Leu	aat Asn	gtc Val	cga Arg	gtg Val	gtc Val	2907

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Pro Glu Gly Val 945 Pro Ser Ala Pro 950 Ser Ser Leu Lys Ile Val Asn Pro 955	
aca ctg gac tct ctc act ttg gaa tgg gat cca ccg agc cac ccg aat	3051
Thr Leu Asp Ser Leu Thr Leu 965 Glu Trp Asp Pro Pro 970 Ser His Pro Asn 970	
ggc att ttg aca gag tac acc tta aag tat cag cca att aac agc aca	3099
Gly Ile Leu Thr Glu Tyr 980 Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr 990 975	
cat gaa tta ggc cct ctg gta gat ttg aaa att cct gcc aac aag aca	3147
His Glu Leu Gly Pro 995 Leu Val Asp Leu Lys 1000 Ile Pro Ala Asn Lys 1005 Thr 1005	
cgg tgg act tta aaa aat tta aat ttc agc act cga tat aag ttt tat	3195
Arg Trp Thr Leu 1010 Lys Asn Leu Asn Phe 1015 Ser Thr Arg Tyr Lys Phe Tyr 1020	
ttc tat gca caa aca tca gca gga tca gga agt caa att aca gag gaa	3243
Phe Tyr Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu 1025 1030 1035	
gca gta aca act gtg gat gaa gct ggt att ctt cca cct gat gta ggt	3291
Ala Val Thr Thr Val Asp 1045 Glu Ala Gly Ile Leu Pro Pro Asp Val Gly 1040 1050	
gca ggc aaa gtt caa gct gta aat acc agg atc agc aat ctt act gct	3339
Ala Gly Lys Val Gln 1060 Val Asn Thr Arg Ile 1065 Ser Asn Leu Thr Ala 1070 1055	
gca gct gct gag acc tat gcc aat atc agt tgg gaa tat gag gga cca	3387
Ala Ala Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro 1075 1080 1085	
gag cat gtg aac ttt tat gtt gaa tat ggt gta gca ggc agc aaa gaa	3435
Glu His Val Asn Phe Tyr Val Glu Tyr Gly Val Ala Gly Ser Lys Glu 1090 1095 1100	
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Glu Trp Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu 1105 1110 1115	
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Lys Gly Leu Met Pro Gly Thr 1125 Ala Tyr Lys Val Arg Val Gly Ala Val 1120 1130	
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Gly Asp Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro 1135 1140 1145 1150	
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Ala Met Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile 1155 1160 1165	
ggt ctg atg tgt gct gtt gct ctc ctt atc tta att ttg ctg att gtt	3675
Gly Leu Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu Leu Ile Val 1170 1175 1180	
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Cys Phe Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val Lys Glu Lys
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Glu Asp Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys Glu Asp Asp
1200 1205 1210

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Gly Thr Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys Pro Leu Lys
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aaa gga agt cga act cct tca gac agg act gtg aaa aaa gaa gat agt 3867
Lys Gly Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys Glu Asp Ser
1235 1240 1245

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Asp Asp Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly Gln Phe Asn
1250 1255 1260

gag gat ggc tcc ttt att gga caa tac agt ggt aag aaa gag aaa gag 3963
Glu Asp Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys Glu Lys Glu
1265 1270 1275

ccg gct gaa gga aac gaa agc tca gag gca cct tct cct gtc aac gcc 4011
Pro Ala Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro Val Asn Ala
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atg aat tcc ttt gtt taa tttttaagct caaagccaat attccatttc 4059
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35 40 45
Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln Cys Glu
50 55 60
Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp Thr Arg Asn Gly Thr
65 70 75 80
His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro Gly Thr
85 90 95
Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly Lys Ala Glu Thr Tyr
100 105 110
Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu Arg Gly Ala Ala Val
115 120 125
Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser Pro Leu Trp Thr Lys

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Asp	Asn	Ser	Phe 180	Gln	Arg	Leu	Pro	Gln 185	Ser	Glu	Arg	Val	Ser 190	Gln	Gly
Leu	Asn	Gly 195	Asp	Leu	Tyr	Phe	Ser 200	Asn	Val	Leu	Pro	Glu 205	Asp	Thr	Arg
Glu 210	Asp	Tyr	Ile	Cys	Tyr	Ala 215	Arg	Phe	Asn	His	Thr 220	Gln	Thr	Ile	Gln
Gln 225	Lys	Gln	Pro	Ile	Ser 230	Val	Lys	Val	Ile	Ser 235	Val	Asp	Glu	Leu	Asn 240
Asp	Thr	Ile	Ala	Ala 245	Asn	Leu	Ser	Asp	Thr 250	Glu	Phe	Tyr	Gly	Ala 255	Lys
Ser	Ser	Arg	Glu 260	Arg	Pro	Pro	Thr	Phe 265	Leu	Thr	Pro	Glu	Gly 270	Asn	Ala
Ser	Asn	Lys 275	Glu	Glu	Leu	Arg	Gly 280	Asn	Val	Leu	Ser	Leu 285	Glu	Cys	Ile
Ala 290	Glu	Gly	Leu	Pro	Thr	Pro 295	Ile	Ile	Tyr	Trp	Ala 300	Lys	Glu	Asp	Gly
Met 305	Leu	Pro	Lys	Asn	Arg 310	Thr	Val	Tyr	Lys	Asn 315	Phe	Glu	Lys	Thr	Leu 320
Gln	Ile	Ile	His	Val 325	Ser	Glu	Ala	Asp	Ser 330	Gly	Asn	Tyr	Gln	Cys 335	Ile
Ala	Lys	Asn	Ala 340	Leu	Gly	Ala	Ile	His 345	His	Thr	Ile	Ser	Val 350	Arg	Val
Lys	Ala	Ala 355	Pro	Tyr	Trp	Ile	Thr 360	Ala	Pro	Gln	Asn	Leu 365	Val	Leu	Ser
Pro	Gly 370	Glu	Asp	Gly	Thr	Leu 375	Ile	Cys	Arg	Ala	Asn 380	Gly	Asn	Pro	Lys
Pro 385	Arg	Ile	Ser	Trp	Leu 390	Thr	Asn	Gly	Val	Pro 395	Ile	Glu	Ile	Ala	Pro 400
Asp	Asp	Pro	Ser	Arg 405	Lys	Ile	Asp	Gly	Asp 410	Thr	Ile	Ile	Phe	Ser 415	Asn
Val	Gln	Glu	Arg 420	Ser	Ser	Ala	Val	Tyr 425	Gln	Cys	Asn	Ala	Ser 430	Asn	Glu
Tyr	Gly	Tyr 435	Leu	Leu	Ala	Asn 440	Phe	Val	Asn	Val	Leu 445	Ala	Glu	Pro	
Pro	Arg 450	Ile	Leu	Thr	Pro	Ala 455	Asn	Thr	Leu	Tyr	Gln 460	Val	Ile	Ala	Asn
Arg 465	Pro	Ala	Leu	Leu	Asp 470	Cys	Ala	Phe	Phe	Gly 475	Ser	Pro	Leu	Pro	Thr 480
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Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala Thr Trp
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 530 535 540
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 545 550 555 560
 Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val Leu Trp
 565 570 575
 Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr Val Asp
 580 585 590
 Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser Gly Thr
 595 600 605
 Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala Ser Ala
 610 615 620
 Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro Ala Pro Val Tyr Asp
 625 630 635 640
 Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu Asp Lys
 645 650 655
 Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser Pro Ile
 660 665 670
 Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro Gly Leu
 675 680 685
 Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala Gln Leu
 690 695 700
 Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala Val Asn
 705 710 715 720
 Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr Leu Thr
 725 730 735
 Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly Leu Gly
 740 745 750
 Ser Glu Pro Asp Asn Leu Glu Ile Thr Trp Lys Pro Leu Asn Gly Phe
 755 760 765
 Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg Gln Lys
 770 775 780
 Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val Ser Lys
 785 790 795 800
 Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile Lys Val
 805 810 815
 Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val Val Met
 820 825 830
 Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn Val Arg
 835 840 845

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Val Asn Val Val Asn Ser Thr Leu Ala Glu Val His Trp Asp Pro Val
850 855 860

Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile Tyr Tyr
865 870 875 880

Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg Arg His Ile Glu Lys
885 890 895

Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu Pro Gly
900 905 910

Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val Asn Gly
915 920 925

Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr Pro Glu
930 935 940

Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro Thr Leu
945 950 955 960

Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn Gly Ile
965 970 975

Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr His Glu
980 985 990

Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr Arg Trp
995 1000 1005

Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr Phe Tyr
1010 1015 1020

Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu Ala Val
1025 1030 1035 1040

Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly Ala Gly
1045 1050 1055

Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala Ala Ala
1060 1065 1070

Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro Glu His
1075 1080 1085

Val Asn Phe Tyr Val Glu Tyr Gly Val Ala Gly Ser Lys Glu Glu Trp
1090 1095 1100

Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu Lys Gly
1105 1110 1115 1120

Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val Gly Asp
1125 1130 1135

Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro Ala Met
1140 1145 1150

Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile Gly Leu
1155 1160 1165

Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu Leu Ile Val Cys Phe
1170 1175 1180

Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val Lys Glu Lys Glu Asp
1185 1190 1195 1200

Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys Glu Asp Asp Gly Thr

20093A-21US-Substitute Sequence Listing.txt
1205 1210 1215

Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys Pro Leu Lys Lys Gly
1220 1225 1230

Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys Glu Asp Ser Asp Asp
1235 1240 1245

Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly Gln Phe Asn Glu Asp
1250 1255 1260

Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys Glu Lys Glu Pro Ala
1265 1270 1275 1280

Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro Val Asn Ala Met Asn
1285 1290 1295

Ser Phe Val

<210> 3
<211> 38
<212> DNA
<213> Homo sapiens

<400> 3
tctcatacta tgaacatatg ggtagagagt atatttttc 38

<210> 4
<211> 123
<212> DNA
<213> Rattus norvegicus

<400> 4
tctcatacta tggacatatg ggtagaaaga atgttttctg cggtatatga gtattataag 60
aacagagcaa gaacataact cagtcagtca gatgatacgt taatatgaac tgggggtgaaa 120
agg 123

<210> 5
<211> 176
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: clone D4-1

<400> 5
tctcatacta tgaacatatg ggtagagagt atatttttctg ctgtatgtta gtattatgag 60
aatagttaca gcaaaaacat aactcagtca aagtatatgt taatatgaac tgggaatgcaa 120
aagtgcatac tttttcattc aaaatgggta ttcttgattt cctaaaaaaaa aaaaaa 176

<210> 6
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 6

20093A-21US-Substitute Sequence Listing.txt 38

tagatacaac tagtcaatgc ctctaatagaa tatggata

<210> 7
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 7
 agatagatcc gcggaatagt aaatccgata gccttgta 38

<210> 8
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
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 <222> (1)
 <223> n=a, c, g, or t

<400> 8
 ngctgctctc atact 15

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 9
 aacatatggg tagagagtat attt 24

<210> 10
 <211> 23
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: primer

<400> 10
 ctttgcattc cagttcatat taa 23

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 11
 tgtggtgaca gatcacggct 20

20093A-21US-Substitute Sequence Listing.txt

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 12
 cagctcaaac ctgtgatttc c 21

 <210> 13
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 13
 aataggtatt ggtgaattta aagactcact ctccataaat gctacgaata ttaaactt 60

 <210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 14
 cggagcaata tgaaatgatc t 21

 <210> 15
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 15
 gcaaatacag ctcctattg 19

 <210> 16
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 16
 gctgtatggt agtattatga gaatagttac agcaaaaaca taa 43

 <210> 17
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>

20093A-21US-Substitute Sequence Listing.txt

<223> Description of Artificial Sequence: primer

<400> 17
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<210> 18
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
tagatacaac tagtctaatag cagcttaaaa taatgcc 37

<210> 19
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
agatagatcc gcggatatcc atattcatta gaggcattg 39

<210> 20
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
tagatacaac tagtcaatgc ctctaataa tatggata 38

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
agatagatcc gcggaatagt aaatccgata gccttgta 38

<210> 22
<211> 61
<212> DNA
<213> Homo sapiens

<220>
<223> Description of Artificial Sequence: primer

<400> 22
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c 61

20093A-21US-Substitute Sequence Listing.txt

<210> 23
 <211> 19
 <212> DNA
 <213> Homo sapiens

 <400> 23
 cattagcatc ttaactcct 19

 <210> 24
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 24
 tcggcattat ttttaagctgc a 21

 <210> 25
 <211> 17
 <212> DNA
 <213> Homo sapiens

 <400> 25
 gcagataagc gcttctt 17

 <210> 26
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 26
 actagagata cagatcatat 20

 <210> 27
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 27
 catatacgat cgatcgatgc 20

 <210> 28
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 28
 gatagtgctg atcgatgcta 20

 <210> 29
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 29
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20093A-21US-Substitute Sequence Listing.txt

<210> 30
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 30
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<210> 31
<211> 1371
<212> DNA
<213> Homo sapiens

<400> 31
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ccaaccatca cccaacagtc tccaaaagat tacattattg accctcggga gaatattgta 180
atccagtgtg aagccaaagg gaaaccgccc ccaagctttt cctggaccgc taatgggact 240
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attaacatca tgagcgaagg gaaagctgag acctatgaag gagtctatca gtgtacagca 360
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ttgtggacca aagaaaaact tgaaccaatc acacttcaaa gtggtcagtc tttagtactt 480
ccctgcagac cccaatttg attaccacca cctataatat tttggatgga taattccttt 540
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caaaccatac agcagaagca acctatttct gtgaagggtga tttcagtgga tgaattgaat 720
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<210> 32
<211> 1371

20093A-21US-Substitute Sequence Listing.txt

<212> DNA

<213> Rattus norvegicus

<400> 32

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ccaactatca ctcaacagtc accaaaagac tacatcattg acccacggga gaatattgta 180
atccaatgtg aggccaaagg gaaacctcct ccaagctttt cctggactcg taacggaaca 240
cattttgaca tagacaaaga ccctctggtc actatgaagc ctggctcagg aacccttgtc 300
atcaacatca tgagtgaagg aaaggcggag acctatgaag gggtttacca gtgcaactgca 360
aggaatgagc gcggagctgc tgtctccaat aacattgttg tccgcccctc taggtcaccc 420
ttgtggacca aggaaagact tgaaccaata atcctccgaa gtggtcagtc actagtacta 480
ccatgtaggc ctccaattgg attaccaccg gccataatat ttggatgga taactccttt 540
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caaacaattc aacagaaaca acctatttct ctgaagggtga tttcagtgga tgaattgaat 720
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<210> 33

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pLXSN MCS (EcoRI and BamHI cloning site)

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36